Resource Summary Report

Generated by NIF on Apr 22, 2025

HIV Databases

RRID:SCR_000614
Type: Tool

Proper Citation

HIV Databases (RRID:SCR_000614)

Resource Information

URL: http://www.hiv.lanl.gov/content/index

Proper Citation: HIV Databases (RRID:SCR_000614)

Description: Contains comprehensive data on HIV genetic sequences and immunological epitopes. This collection of databases contains tools to visualize and analyze HIV-related data.

Resource Type: data or information resource, database, software resource

Keywords: HIV, AIDS, HIV genetic sequences and immunological epitopes data, tools to visualize and analyze HIV-related data, FASEB list

Related Condition: HIV, AIDS, SIV

Funding: NIAID

Resource Name: HIV Databases

Resource ID: SCR_000614

Alternate IDs: SCR_014940, nlx_151409

Record Creation Time: 20220129T080202+0000

Record Last Update: 20250422T054910+0000

Ratings and Alerts

No rating or validation information has been found for HIV Databases.

No alerts have been found for HIV Databases.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 495 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Sahoo A, et al. (2022) Structure-guided changes at the V2 apex of HIV-1 clade C trimer enhance elicitation of autologous neutralizing and broad V1V2-scaffold antibodies. Cell reports, 38(9), 110436.

Chen S, et al. (2018) Twenty-seven year surveillance of blood transfusion recipients infected with HIV-1 in Hebei Province, China. PloS one, 13(8), e0202265.

Zhao S, et al. (2018) Prevalence of Transmitted HIV drug resistance in antiretroviral treatment naïve newly diagnosed individuals in China. Scientific reports, 8(1), 12273.

Yang Y, et al. (2018) Phylogenetic and temporal dynamics of human immunodeficiency virus type 1 CRF01_AE and CRF07_BC among recently infected antiretroviral therapy-naïve men who have sex with men in Jiangsu province, China, 2012 to 2015: A molecular epidemiology-based study. Medicine, 97(6), e9826.

Eccleston RC, et al. (2017) Host genotype and time dependent antigen presentation of viral peptides: predictions from theory. Scientific reports, 7(1), 14367.

Guo J, et al. (2017) Genetic characterization and antiretroviral resistance mutations among treatment-naive HIV-infected individuals in Jiaxing, China. Oncotarget, 8(11), 18271.

Jiang X, et al. (2017) Protein structural disorder of the envelope V3 loop contributes to the switch in human immunodeficiency virus type 1 cell tropism. PloS one, 12(10), e0185790.

Ghimire D, et al. (2017) Insights into the activity of maturation inhibitor PF-46396 on HIV-1 clade C. Scientific reports, 7, 43711.

Lu X, et al. (2017) HIV-1 molecular epidemiology among newly diagnosed HIV-1 individuals in Hebei, a low HIV prevalence province in China. PloS one, 12(2), e0171481.

Carneiro J, et al. (2017) The HIV oligonucleotide database (HIVoligoDB). Database : the journal of biological databases and curation, 2017(1).

Lu Z, et al. (2016) Identifying possible sites for antibody neutralization escape: Implications for unique functional properties of the C-terminal tail of Human Immunodeficiency Virus Type 1 gp41. Immunology letters, 175, 21.

Qu D, et al. (2016) The variances of Sp1 and NF-?B elements correlate with the greater capacity of Chinese HIV-1 B'-LTR for driving gene expression. Scientific reports, 6, 34532.

Johnson AL, et al. (2016) A Highly Conserved Residue in HIV-1 Nef Alpha Helix 2 Modulates Protein Expression. mSphere, 1(6).

Timilsina U, et al. (2016) Identification of potent maturation inhibitors against HIV-1 clade C. Scientific reports, 6, 27403.

McCoy LE, et al. (2016) Holes in the Glycan Shield of the Native HIV Envelope Are a Target of Trimer-Elicited Neutralizing Antibodies. Cell reports, 16(9), 2327.

Scharf L, et al. (2016) Structural basis for germline antibody recognition of HIV-1 immunogens. eLife, 5.

Liu Z, et al. (2015) The highly polymorphic cyclophilin A-binding loop in HIV-1 capsid modulates viral resistance to MxB. Retrovirology, 12, 1.

Han X, et al. (2015) A Large-scale Survey of CRF55_01B from Men-Who-Have-Sex-with-Men in China: implying the Evolutionary History and Public Health Impact. Scientific reports, 5, 18147.

Jia L, et al. (2015) A considerable proportion of CRF01_AE strains in China originated from circulating intrasubtype recombinant forms (CIRF). BMC infectious diseases, 15, 528.

Li X, et al. (2015) HIV-1 Genetic Diversity and Its Impact on Baseline CD4+T Cells and Viral Loads among Recently Infected Men Who Have Sex with Men in Shanghai, China. PloS one, 10(6), e0129559.